It is estimated that infection accounts for 15% of all cancers globally. The involvement of *Helicobacter pylori* in over 90% of gastric noncardia adenocarcinoma and the role of Human Papillomavirus in cervical tumorigenesis are testament to the prominent role that pathogens play in cancer. As we transition into an era of genomic medicine, it is becoming increasingly possible to characterise the tumour-microbe landscape by interrogating high-throughput sequencing data.

We have developed a computational pipeline (SEPATH) as a benchmarked approach to report the metagenomic constituents found within human tissue samples. SEPATH is being applied to tumour samples from within Genomics England’s 100,000 Genomes Project. The resulting data is highly sparse in nature and rife with environmental contaminants. Despite this, SEPATH has revealed a range of interesting bacterial and viral genera associated with tumour samples, particularly in colorectal tumours. Many of the genera identified have been previously suggested for association with tumours such as *Bacteroides* and *Fusobacterium* in colorectal cancer and *Alphapapillomavirus* in oral cancer. Additionally, we have detected evidence for infectious disease which will be subject to independent validation and followed up appropriately.

Analysing the microbial composition of tumours could provide an additional tool to aid in therapeutic stratification of cancer patients with little added cost following sequencing. Additionally, novel treatment avenues could be investigated further such as the use of antibiotics in certain types of cancer. The dataset will be interrogated further for potential relationships between taxa and clinical variables as increasing amounts of clinical data becomes available.